CLUSTAL W (1.83) multiple sequence alignment

gi|4454552|gb|AAD20946.1| = SEQ ID NO:5
gi|1045655|gb|AAC50236.1| = Sequence from Chen et al.

```
gi|4454552|gb|AAD20946.1|   MSGSTQLVAQTWRATBPRYPPHSLSYPVQIARTHTDVGLLEYQHHSRDYA   50
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                                           :  :    :::

gi|4454552|gb|AAD20946.1|   SHLSPGSIIQPQRRRPSLLSEFQPGNERSQELHLRPESHSYLPELGKSEM  100
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            :    ::                           ::          :

gi|4454552|gb|AAD20946.1|   BFIBSKRPRLELLPDPLLRPSPLLATGQPAGSEDLTKDRSLTGKLEPVSP  150
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            ::          ::    ::      :

gi|4454552|gb|AAD20946.1|   PSPPHTDPELELVPPRLSKEELIQNMDRVDREITMVEQQISKLKKKQQQL  200
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                                 ::    ::     :    ::  ::        :   :

gi|4454552|gb|AAD20946.1|   EEEAAKPPBPEKPVSPPPIESKHRSLVQIIYDENRKKABAAHRILBGLGP  250
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                                :              :       :: ::        ::  :

gi|4454552|gb|AAD20946.1|   QVELPLYNQPSDTRQYHENIKINQAMRKKLILYFKRRNHARKQWKQKPCQ  300
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            : :                         ::: :        :

gi|4454552|gb|AAD20946.1|   RYDQLMEALEKKVERIENNPRRRAKESKVREYYEKQFPBIRKQRELQERM  350
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            ::  :        :   :               :       ::

gi|4454552|gb|AAD20946.1|   QSRVGQRGSGLSMSAARSEHEVSEIIDGLSEQENLEKQMRQLAVIPPMLY  400
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            : :           ::    ::: :      :   :

gi|4454552|gb|AAD20946.1|   DADQQRIKFINMNGLMADPMKVYKDRQVMNMWSEQEKETFREKFMQHPKN  450
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            : :::  ::      ::             :            ::

gi|4454552|gb|AAD20946.1|   FGLIASFLERKTVAECVLYYYIJTKKNENYKSLVRRSYRRGKSQQQQQQQ  500
gi|1045655|gb|AAC50236.1|   --------------------------------------------------
                            :  ::    :     ::          :              ::
```

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```
gi|4454552|gb|AAD20946.1|  QQQQQQQQQPMPRSSQREKDEKEKEKEABKEBEKPEVENDKEDLLKEKT 550
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  DDTSGEDNDEKEAVASKGRKTANSQGRRKGRITRSMANEANSEEAITPQQ 600
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  SAELASMELMESSRWTEEEMETAKKGLLEHGRNWSAIARMVGSKTVSQCK 650
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  NFYFNYKKRQNLDEILQQHKLKMEKEFNARRKKKKAPAAASEEAAFPPVV 700
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  EDEBMEASGVSGNEEEMVEEAEALHASGNEVPRGECSGPATVNNSSDTES 750
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  IPSPHTEAAKDTGQNGPKPPATLGADGPPPGPPTPPRRTSRAPIEPTPAS 800
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  EATGAPTPPPAPPSPSAPPVVPKEBKEEETAAAPPVEBGEEQKPPAAEE 850
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  LAVDTGKAEEPVKSECTEEAEGPAKGKDAEAAEATAEGALKABKKEGGS 900
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  GRATTAKSSGAPQDSDSSATCSADBVDEABGGDKNRLLSPRPSLLTPTGD 950
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  PRANASPQKPIDLKQLKQRAAAIPPIQVTKVHBPPREDAAPTKPAPPAPP 1000
gi|1045655|gb|AAC50236.1|

gi|4454552|gb|AAD20946.1|  PPQNLQPBSDAPQQPGSSPRGKSRSPAPPADKEAPAAEAQKLPGDPPCWT 1050
gi|1045655|gb|AAC50236.1|  MEAWDAHPDKEAFAAEAQKLPGDPPCWT 28
                                                      ****************
```

2

DLMR_292270.1

```
gi|4454552|gb|AAD20946.1|  SGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPP 1100
gi|1045655|gb|AAC50236.1|  SGLPFPVPPREVIKASPHAPDPSAFSYAPPGHPLPLGLHDTARPVLPRPP 78
                           **************************************************

gi|4454552|gb|AAD20946.1|  TISNPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTM 1150
gi|1045655|gb|AAC50236.1|  TISNPPLISSAKHPSVLERQIGAISQGMSVQLHVPYSEHAKAPVGPVTM 128
                           *************************************************

gi|4454552|gb|AAD20946.1|  GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTAL 1200
gi|1045655|gb|AAC50236.1|  GLPLPMDPKKLAPFSGVKQEQLSPRGQAGPPESLGVPTAQEASVLRGTAL 178
                           **************************************************

gi|4454552|gb|AAD20946.1|  GSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGED 1250
gi|1045655|gb|AAC50236.1|  GSVPGGSITKGIPSTRVPSDSAITYRGSITHGTPADVLYKGTITRIIGED 228
                           **************************************************

gi|4454552|gb|AAD20946.1|  SPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGP 1300
gi|1045655|gb|AAC50236.1|  SPSRLDRGREDSLPKGHVIYEGKKGHVLSYEGGMSVTQCSKEDGRSSSGP 278
                           **************************************************

gi|4454552|gb|AAD20946.1|  PHETAAPKRTYDMWEGRVGRAISSASIEGLMGRAIPPBRHSPHHLKEQHH 1350
gi|1045655|gb|AAC50236.1|  PHETAAPKRTYDMWEGRVGRAISSASIEGLMGRAIPPBRHSPHRLKEQHH 328
                           **************************************************

gi|4454552|gb|AAD20946.1|  IRGSITQGIPRSVVEAQEDYLRREAKLLKREGTPPPPSRDLTBAYKTQ 1400
gi|1045655|gb|AAC50236.1|  IRGSITQGIPRSVVEAQEDYLRREAKLLKREGTPPPPSRDLTBAYKTQ 378
                           ************************************************

gi|4454552|gb|AAD20946.1|  ALGPLKLKPAHEGLVATVKEAGRSIHEIPRBELRHTPBLPLAPRPLKEGS 1450
gi|1045655|gb|AAC50236.1|  ALGPLKLKPAHEGLVATVKEAGRSIHEIPRBELRHTPELPLAPRPLKEGS 428
                           **************************************************

gi|4454552|gb|AAD20946.1|  ITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALE 1500
gi|1045655|gb|AAC50236.1|  ITQGTPLKYDTGASTTGSKKHDVRSLIGSPGRTFPPVHPLDVMADARALE 478
                           **************************************************

gi|4454552|gb|AAD20946.1|  RACYEBSLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPF 1550
gi|1045655|gb|AAC50236.1|  RACYEESLKSRPGTASSSGGSIARGAPVIVPELGKPRQSPLTYEDHGAPF 528
                           **************************************************

gi|4454552|gb|AAD20946.1|  AGHLPRGSPVTMREPTPRLQEGSLSSSKASQDRKLTSTPREIAKSPHSTV 1600
gi|1045655|gb|AAC50236.1|  AGHLPRGSPVTMREPTPRLQEGSLSSSKASQDRKLTSTPRBIAKSPHSTV 578
                           **************************************************
```

3

DLMR_292270.1

gi|4454552|gb|AAD20946.1| PEHHPHPISPYEHLLRGVSGGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYY 1650
gi|1045655|gb|AAC50236.1| PEHHPHPISPYEHLLRGVSGGVDLYRSHIPLAFDPTSIPRGIPLDAAAAYY 628
                             ****

gi|4454552|gb|AAD20946.1| LPRHLAPNPTYPHLYPPYLLRGYPDTAALENRQTIINDYITSQQMHRNTA 1700
gi|1045655|gb|AAC50236.1| LPRHLAPNPTYPHLYPPYLLRGYPDTAALENRQTIINDYITSQQMHRNTA 678
                             ****

gi|4454552|gb|AAD20946.1| TAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGT 1750
gi|1045655|gb|AAC50236.1| TAMAQRADMLRGLSPRESSLALNYAAGPRGIIDLSQVPHLPVLVPPTPGT 728
                             ****

gi|4454552|gb|AAD20946.1| PATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSRERDR 1800
gi|1045655|gb|AAC50236.1| PATAMDRLAYLPTAPQPFSSRHSSSPLSPGGPTHLTKPTTTSSSRERDR 778
                             ****

gi|4454552|gb|AAD20946.1| DRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSR 1850
gi|1045655|gb|AAC50236.1| DRERDRDREREKSILTSTTTVEHAPIWRPGTEQSSGSSGSSGGGGSSSR 828
                             ****

gi|4454552|gb|AAD20946.1| PASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRS 1900
gi|1045655|gb|AAC50236.1| PASHSHAHQHSPISPRTQDALQQRPSVLHNTGMKGIITAVEPSKPTVLRS 878
                             ****

gi|4454552|gb|AAD20946.1| TSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPER 1950
gi|1045655|gb|AAC50236.1| TSTSSPVRPAATFPPATHCPLGGTLDGVYPTLMEPVLLPKEAPRVARPER 928
                             ****

gi|4454552|gb|AAD20946.1| PRADTGHAFLAKPPARSGLEPASSPSKGSRPRPLVPPVSGHATIARTPAK 2000
gi|1045655|gb|AAC50236.1| PRADTGHAFLAKPPARSGLEPASSPSKGSRPRPLVPPVSGHATIARTPAK 978
                             ****

gi|4454552|gb|AAD20946.1| NLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSP 2050
gi|1045655|gb|AAC50236.1| NLAPHHASPDPPAPPASASDPHREKTQSKPFSIQELELRSLGYHGSSYSP 1028
                             ****

gi|4454552|gb|AAD20946.1| EGVEPVSPVSSPSLTHDKGLPKHLELDKSHLEGELRPKQPGPVKLGGEA 2100
gi|1045655|gb|AAC50236.1| EGVEPVSPVSSPSLTHDKGLPKHLELDKSHLEGELRPKQPGPVKLGGEA 1078
                             ****

gi|4454552|gb|AAD20946.1| AHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRH 2150
gi|1045655|gb|AAC50236.1| AHLPHLRPLPESQPSSSPLLQTAPGVKGHQRVVTLAQHISEVITQDYTRH 1128

4

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```
gi|4454552|gb|AAD20946.1|    HPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHS  2200
gi|1045655|gb|AAC50236.1|    HPQQLSAPLPAPLYSFPGASCPVLDLRRPPSDLYLPPPDHGAPARGSPHS  1178
                            **************************************************

gi|4454552|gb|AAD20946.1|    EGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGE  2250
gi|1045655|gb|AAC50236.1|    EGGKRSPEPNKTSVLGGGEDGIEPVSPPEGMTEPGHSRSAVYPLLYRDGE  1228
                            **************************************************

gi|4454552|gb|AAD20946.1|    QTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQBINKKLNTHNRN  2300
gi|1045655|gb|AAC50236.1|    QTEPSRMGSKSPGNTSQPPAFFSKLTESNSAMVKSKKQBINKKLNTHNRN  1278
                            **************************************************

gi|4454552|gb|AAD20946.1|    EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKAL  2350
gi|1045655|gb|AAC50236.1|    EPEYNISQPGTEIFNMPAITGTGLMTYRSQAVQEHASTNMGLEAIIRKAL  1328
                            **************************************************

gi|4454552|gb|AAD20946.1|    MGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG  2400
gi|1045655|gb|AAC50236.1|    MGKYDQWEESPPLSANAFNPLNASASLPAAMPITAADGRSDHTLTSPGGG  1378
                            **************************************************

gi|4454552|gb|AAD20946.1|    GKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVW  2450
gi|1045655|gb|AAC50236.1|    GKAKVSGRPSSRKAKSPAPGLASGDRPPSVSSVHSEGDCNRRTPLTNRVW  1428
                            **************************************************

gi|4454552|gb|AAD20946.1|    EDRPSSAGSTPFFYNPLIMRLQAGVMASPPPPGLPAGSGPLAGPHHAWDE  2500
gi|1045655|gb|AAC50236.1|    EDRPSSAGSTPFFYNPLIMRLQAGVMASPPPPGLPAGSGPLAGPHHAWDE  1478
                            **************************************************

gi|4454552|gb|AAD20946.1|    EPKPLLCSQYETL8DSE  2517
gi|1045655|gb|AAC50236.1|    EPKPLLCBQYETLSDSE  1495
                            ****************
```

5

DLMR_292270.1